

#6

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING**

### **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/537,562  
Source: PCR  
Date Processed by STIC: 2/10/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT; WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/537,562

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
           Wrapped Aminos    The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2        Invalid Line Length    The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3        Misaligned Amino  
           Numbering        The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4        Non-ASCII            The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5        Variable Length      Sequence(s)        contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6        PatentIn 2.0  
           "bug"                A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7        Skipped Sequences  
    (OLD RULES)            Sequence(s)        missing. If intentional, please insert the following lines for **each** skipped sequence:  
                                  (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                  (i)        SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                                  (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                                  This sequence is intentionally skipped  
  
                                  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8        Skipped Sequences  
    (NEW RULES)            Sequence(s)        missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                                  <210> sequence id number  
                                  <400> sequence id number  
                                  000
  
- 9        Use of n's or Xaa's  
    (NEW RULES)            Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                                  Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                                  In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10        Invalid <213>  
    Response                Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11        Use of <220>        Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses.  
                                  Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                                  (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12        PatentIn 2.0  
           "bug"                Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13        Misuse of n/Xaa      "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

**BEST AVAILABLE COPY**



PCT

## RAW SEQUENCE LISTING

DATE: 02/10/2006

PATENT APPLICATION: US/10/537,562

TIME: 08:44:17

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\02102006\J537562.raw

*see item 4 on Euro  
Summary Sheet*

base

3 <110> APPLICANT: bioMerieux B.V.  
4 Venema, Fokke

6 <120> TITLE OF INVENTION: Method for lowering both sequence variations and increase of  
7 line's effects in a diagnostic hybridisation assay, assay for  
8 performing such a method and probe for use in the assay

10 <130> FILE REFERENCE: L/2AR80/MK/57

C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/537,562

C--> 12 <141> CURRENT FILING DATE: 2005-06-03

12 <150> PRIOR APPLICATION NUMBER: EP 02 080 125.4

13 <151> PRIOR FILING DATE: 2002-12-03

15 <160> NUMBER OF SEQ ID NOS: 13

17 <170> SOFTWARE: PatentIn version 3.2

19 <210> SEQ ID NO: 1

20 <211> LENGTH: 26

21 <212> TYPE: DNA

22 <213> ORGANISM: Artificial

24 <220> FEATURE:

25 <223> OTHER INFORMATION: Ref

28 <220> FEATURE:

29 <221> NAME/KEY: modified\_base

30 <222> LOCATION: (1)..(26)

31 <223> OTHER INFORMATION: I

33 <220> FEATURE:

34 <221> NAME/KEY: misc\_feature

35 <222> LOCATION: (1)..(26)

36 <223> OTHER INFORMATION: n = inosine

38 <400> SEQUENCE: 1

39 atcaatgagg angctgcaga ntggga

42 <210> SEQ ID NO: 2

43 <211> LENGTH: 26

44 <212> TYPE: DNA

45 <213> ORGANISM: Artificial

47 <220> FEATURE:

48 <223> OTHER INFORMATION: Me-1

51 <220> FEATURE:

52 <221> NAME/KEY: misc\_feature

53 <222> LOCATION: (1)..(26)

54 <223> OTHER INFORMATION: n = inosine; r = 2'-O-Me nucleotide of a

56 <220> FEATURE:

57 <221> NAME/KEY: modified\_base

58 <222> LOCATION: (1)..(26)

59 <223> OTHER INFORMATION: 2'-O-methyladenosine

61 <400> SEQUENCE: 2

*Please give source of genetic material (see item 11 on Euro Summary Sheet)*

*delete you don't need this, since I'm represented by "n" and explained*

*Does Not Comply Corrected Diskette Needed*

*give source*

*Per Sequence Rules "r" represents a or g*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/537,562

DATE: 02/10/2006

TIME: 08:44:17

Input Set : A:\PTO.RJ.txt

Output Set : N:\CRF4\02102006\J537562.raw

W--&gt; 62 atcrrtgrgg rngctgcrgr ntggga

26

65 &lt;210&gt; SEQ ID NO: 3

66 &lt;211&gt; LENGTH: 26

67 &lt;212&gt; TYPE: DNA

68 &lt;213&gt; ORGANISM: Artificial

70 &lt;220&gt; FEATURE:

71 &lt;223&gt; OTHER INFORMATION: Me-2

74 &lt;220&gt; FEATURE:

75 &lt;221&gt; NAME/KEY: misc\_feature

76 &lt;222&gt; LOCATION: (1)..(26)

77 &lt;223&gt; OTHER INFORMATION: n = inosine nucleotide of g

78 of g

80 &lt;220&gt; FEATURE:

81 &lt;221&gt; NAME/KEY: modified\_base

82 &lt;222&gt; LOCATION: (1)..(26)

83 &lt;223&gt; OTHER INFORMATION: gm

85 &lt;220&gt; FEATURE:

86 &lt;221&gt; NAME/KEY: modified\_base

87 &lt;222&gt; LOCATION: (1)..(26)

88 &lt;223&gt; OTHER INFORMATION: I

90 &lt;220&gt; FEATURE:

91 &lt;221&gt; NAME/KEY: modified\_base

92 &lt;222&gt; LOCATION: (1)..(26)

93 &lt;223&gt; OTHER INFORMATION: 2'-O-methyladenosine

95 &lt;400&gt; SEQUENCE: 3

W--&gt; 96 atcrrtkakk rnkctkcakr ntkkga

26

99 &lt;210&gt; SEQ ID NO: 4

100 &lt;211&gt; LENGTH: 26

101 &lt;212&gt; TYPE: DNA

102 &lt;213&gt; ORGANISM: Artificial

104 &lt;220&gt; FEATURE:

105 &lt;223&gt; OTHER INFORMATION: Me-7

108 &lt;220&gt; FEATURE:

109 &lt;221&gt; NAME/KEY: misc\_feature

110 &lt;222&gt; LOCATION: (1)..(26)

111 &lt;223&gt; OTHER INFORMATION: n = inosine nucleotide of g

112 of g

114 &lt;220&gt; FEATURE:

115 &lt;221&gt; NAME/KEY: modified\_base

116 &lt;222&gt; LOCATION: (1)..(26)

117 &lt;223&gt; OTHER INFORMATION: 2'-O-methyladenosine

119 &lt;220&gt; FEATURE:

120 &lt;221&gt; NAME/KEY: modified\_base

121 &lt;222&gt; LOCATION: (1)..(26)

122 &lt;223&gt; OTHER INFORMATION: gm OK

124 &lt;220&gt; FEATURE:

125 &lt;221&gt; NAME/KEY: modified\_base

126 &lt;222&gt; LOCATION: (1)..(26)

127 &lt;223&gt; OTHER INFORMATION: I

already explained above

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/537,562

DATE: 02/10/2006

TIME: 08:44:17

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\02102006\J537562.raw

129 <400> SEQUENCE: 4  
W--> 130 atcrrtkakk rnkctkcrkr ntkkka 26  
133 <210> SEQ ID NO: 5  
134 <211> LENGTH: 26  
135 <212> TYPE: DNA  
136 <213> ORGANISM: Artificial  
138 <220> FEATURE:  
139 <223> OTHER INFORMATION: Ref2  
141 <400> SEQUENCE: 5  
142 atcaatgagg aagctgcaga atggga 26  
145 <210> SEQ ID NO: 6  
146 <211> LENGTH: 26  
147 <212> TYPE: DNA  
148 <213> ORGANISM: Artificial  
150 <220> FEATURE:  
151 <223> OTHER INFORMATION: LNA1  
154 <220> FEATURE:  
155 <221> NAME/KEY: misc\_feature  
156 <222> LOCATION: (1)..(26)  
157 <223> OTHER INFORMATION: b = LNA nucleotide of a; w = LNA nucleotide of t W = a or t  
159 <400> SEQUENCE: 6  
160 btcaatgagg aagcwgacaga atggga 26  
163 <210> SEQ ID NO: 7  
164 <211> LENGTH: 26  
165 <212> TYPE: DNA  
166 <213> ORGANISM: Artificial  
168 <220> FEATURE:  
169 <223> OTHER INFORMATION: LNA2  
172 <220> FEATURE:  
173 <221> NAME/KEY: misc\_feature  
174 <222> LOCATION: (1)..(26)  
175 <223> OTHER INFORMATION: b = LNA nucleotide of a; w = LNA nucleotide of t  
177 <400> SEQUENCE: 7  
178 btcaatgagg bagcwgacaga atggga 26  
181 <210> SEQ ID NO: 8  
182 <211> LENGTH: 26  
183 <212> TYPE: DNA  
184 <213> ORGANISM: Artificial  
186 <220> FEATURE:  
187 <223> OTHER INFORMATION: Ref. molecular beacon  
190 <220> FEATURE:  
191 <221> NAME/KEY: misc\_feature  
192 <222> LOCATION: (1)..(26)  
193 <223> OTHER INFORMATION: n = inosine  
195 <220> FEATURE:  
196 <221> NAME/KEY: modified\_base  
197 <222> LOCATION: (1)..(26)  
198 <223> OTHER INFORMATION: I  
200 <400> SEQUENCE: 8

*b = c or g or t/u, not a*

*W = a or t*

*delete - already shown above*

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/537,562

DATE: 02/10/2006

TIME: 08:44:17

Input Set : A:\PTO.RJ.txt

Output Set : N:\CRF4\02102006\J537562.raw

W--> 201 atcaatgagg angctgcaga ntggga 26

204 <210> SEQ ID NO: 9

205 <211> LENGTH: 26

206 <212> TYPE: DNA

207 <213> ORGANISM: Artificial

209 <220> FEATURE:

210 <223> OTHER INFORMATION: Subtype A

213 <220> FEATURE:

214 <221> NAME/KEY: misc\_feature

215 <222> LOCATION: (1)..(26)

216 <223> OTHER INFORMATION: r = 2'-O-Me nucleotide of a

218 <220> FEATURE:

219 <221> NAME/KEY: modified\_base

220 <222> LOCATION: (1)..(26)

221 <223> OTHER INFORMATION: 2'-O-methyladenosine

223 <400> SEQUENCE: 9

224 atcaatgagg argctgcaga rtggga 26

227 <210> SEQ ID NO: 10

228 <211> LENGTH: 26

229 <212> TYPE: DNA

230 <213> ORGANISM: Artificial

232 <220> FEATURE:

233 <223> OTHER INFORMATION: Subtype G1

236 <220> FEATURE:

237 <221> NAME/KEY: misc\_feature

238 <222> LOCATION: (1)..(26)

239 <223> OTHER INFORMATION: r = 2'-O-Me nucleotide of a; k = 2'-O-Me nucleotide of g v

240 2'-O-nucleotide of t V = a or c or g

242 <220> FEATURE:

243 <221> NAME/KEY: modified\_base

244 <222> LOCATION: (1)..(26)

245 <223> OTHER INFORMATION: 2'-O-methyladenosine

247 <220> FEATURE:

248 <221> NAME/KEY: modified\_base

249 <222> LOCATION: (1)..(26)

250 <223> OTHER INFORMATION: gm

252 <220> FEATURE:

253 <221> NAME/KEY: modified\_base

254 <222> LOCATION: (1)..(26)

255 <223> OTHER INFORMATION: 2'-O-methylthymidine

257 <400> SEQUENCE: 10

258 atvaatgarg argctgcaga ktggga 26

261 <210> SEQ ID NO: 11

262 <211> LENGTH: 26

263 <212> TYPE: DNA

264 <213> ORGANISM: Artificial

266 <220> FEATURE:

267 <223> OTHER INFORMATION: Subtype N

270 <220> FEATURE:

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/537,562

DATE: 02/10/2006

TIME: 08:44:17

Input Set : A:\PTO.RJ.txt

Output Set : N:\CRF4\02102006\J537562.raw

271 <221> NAME/KEY: misc\_feature  
 272 <222> LOCATION: (1)..(26)  
 273 <223> OTHER INFORMATION: r = 2'-O-Me nucleotide of a; d = 2'-O-Me nucleotide of c  
 275 <220> FEATURE:  
 276 <221> NAME/KEY: modified\_base  
 277 <222> LOCATION: (1)..(26)  
 278 <223> OTHER INFORMATION: 2'-O-methyladenosine  
 280 <220> FEATURE:  
 281 <221> NAME/KEY: modified\_base  
 282 <222> LOCATION: (1)..(26)  
 283 <223> OTHER INFORMATION: cm  
 285 <400> SEQUENCE: 11  
 286 atcaatgagg argcrgcaga dtggga 26  
 289 <210> SEQ ID NO: 12  
 290 <211> LENGTH: 26  
 291 <212> TYPE: DNA  
 292 <213> ORGANISM: Artificial  
 294 <220> FEATURE:  
 295 <223> OTHER INFORMATION: Subtype O1  
 298 <220> FEATURE:  
 299 <221> NAME/KEY: misc\_feature  
 300 <222> LOCATION: (1)..(26)  
 301 <223> OTHER INFORMATION: r = 2'-O-Me nucleotide of a; v = 2'-O-Me nucleotide of t  
 303 <220> FEATURE:  
 304 <221> NAME/KEY: modified\_base  
 305 <222> LOCATION: (1)..(26)  
 306 <223> OTHER INFORMATION: 2'-O-methyladenosine  
 308 <220> FEATURE:  
 309 <221> NAME/KEY: modified\_base  
 310 <222> LOCATION: (1)..(26)  
 311 <223> OTHER INFORMATION: 2'-O-methylthymidine  
 313 <400> SEQUENCE: 12  
 314 atcaatgavg argcrgcaga vtggga 26  
 317 <210> SEQ ID NO: 13  
 318 <211> LENGTH: 26  
 319 <212> TYPE: DNA  
 320 <213> ORGANISM: Artificial  
 322 <220> FEATURE:  
 323 <223> OTHER INFORMATION: Subtype O3  
 326 <220> FEATURE:  
 327 <221> NAME/KEY: misc\_feature  
 328 <222> LOCATION: (1)..(26)  
 329 <223> OTHER INFORMATION: r = 2'-O-Me nucleotide of a; k = 2'-O-Me nucleotide of g; v  
 330 2'-O-Me nucleotide of t  
 332 <220> FEATURE:  
 333 <221> NAME/KEY: modified\_base  
 334 <222> LOCATION: (1)..(26)  
 335 <223> OTHER INFORMATION: 2'-O-methyladenosine  
 337 <220> FEATURE:

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/537,562

DATE: 02/10/2006  
TIME: 08:44:18

Input Set : A:\PTO.RJ.txt  
Output Set: N:\CRF4\02102006\J537562.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 12,21  
Seq#:2; N Pos. 12,21  
Seq#:3; N Pos. 12,21  
Seq#:4; N Pos. 12,21  
Seq#:8; N Pos. 12,21

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13



**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/537,562

DATE: 02/10/2006

TIME: 08:44:18

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\02102006\J537562.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:39 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0  
L:62 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0  
L:96 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0  
L:130 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0  
L:201 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0